

SPRI/XREFdb BLAST Report xrBLAST4371643066_0

This BLAST Search was run Jun 23 1997 12:47:57

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= **EPLEPSILON**
(219 letters)

Database: /data/datasets/nt
329,017 sequences; 497,918,314 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

from this report into SPRI/XREFdb

AD

Sequences Producing High Segment Pairs		Frame	Score	P(N)	N
gi 33798 emb X645...	H.sapiens gene for interleukin-1 receptor ant...	0	259	5.8e-05	1
gi 587699 gb I095...	Sequence 1 from Patent WO 8911540	0	239	0.00011	1
gi 587700 gb I095...	Sequence 3 from Patent WO 8911540	0	239	0.00011	1
gi 1008970 emb X8...	H.sapiens mRNA for intracellular IL-1 recepto...	0	239	0.00014	1
gi 587702 gb I095...	Sequence 8 from Patent WO 8911540 >gi 589153 ...	0	239	0.00015	1
gi 186291 gb M556...	Human icIL-1ra mRNA, complete cds.	0	239	0.00015	1
gi 186385 gb M630...	Human interleukin 1 receptor antagonist (IL1R...	0	230	0.00031	1
gi 32578 emb X532...	H.sapiens mRNA for IRAP	0	239	0.00036	1
gi 32576 emb X520...	H.sapiens mRNA for interleukin-1 receptor ant...	0	239	0.00037	1
gi 1567289 emb A3...	Synthetic (50Gly,51Gly) IL-1 beta gene	0	206	0.0033	1
gi 1567283 emb A3...	Synthetic IL-1 beta gene	0	206	0.0034	1
gi 1567285 emb A3...	Synthetic (63Ser,65Ser) IL-1beta	0	206	0.0034	1

SPRI/XREFdb BLAST Report xrBLAST1174926757_0

This BLAST Search was run Jun 23 1997 13:44:40

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= **IL1DELTA**
(470 letters)

Database: /data/dataset **SPRI**
329,017 sequences; 497,918,314 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done

from this report into SPRI/XREFdb

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
AF gi 545740 gb S689...	sIL-1ra=interleukin-1 receptor antagonist sec...	0	476	1.1e-15	1
gi 425787 dbj D21...	Rabbit mRNA for interleukin 1 receptor antago...	0	467	1.2e-14	1
gi 165436 gb M575...	Rabbit interleukin 1 receptor antagonist (IL1...	0	467	1.2e-14	1
gi 186291 gb M556...	Human icIL-1ra mRNA, complete cds.	0	446	2.4e-14	1
gi 587702 gb I095...	Sequence 8 from Patent WO 8911540 >gi 589153 ...	0	446	2.4e-14	1
gi 1008970 emb X8...	H.sapiens mRNA for intracellular IL-1 recepto...	0	446	2.5e-14	1
gi 587699 gb I095...	Sequence 1 from Patent WO 8911540	0	446	2.6e-14	1
gi 587700 gb I095...	Sequence 3 from Patent WO 8911540	0	446	2.6e-14	1
gi 186385 gb M630...	Human interleukin 1 receptor antagonist (IL1R...	0	446	2.7e-14	1
gi 238584 gb S640...	interleukin 1 receptor antagonist protein [mi...	0	442	4.0e-14	1

SPRI/XREFdb BLAST Report xrBLAST9122009277_0

 This BLAST Search was run Jun 23 1997 14:10:53

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
 Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
 Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
 nearly identical sequences rapidly. To identify weak similarities encoded in
 nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= **EEIEPSILON**
 (219 letters)

Database: /data/datasets/est
 1,082,928 sequences; 395,818,522 total letters.
 Searching....10....20....30....40....50....60....70....80....90....100% done

 from this report into SPRI/XREFdb

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi 1497479 gb AA0...mi08c10.r1 Soares mouse placenta	0	1095	1.2e-43	1	
4NbMPL3.5 14...					
gi 1388557 gb W78...zd72d01.r1 Soares fetal heart	0	248	2.3e-05	1	
NbHH19W Homo sa...					
gi 812143 gb R502...yj58a03.r1 Homo sapiens cDNA	0	229	0.00026	1	
clone 152908 5' ...					
gi 806268 gb R468...yj54f05.r1 Homo sapiens cDNA	0	223	0.00052	1	
clone 152577 5' ...					
gi 2034114 gb AA3...EST94914 Activated T-cells I	0	183	0.028	1	
Homo sapiens cDN...					
gi 1693322 gb AA1...zl35f02.r1 Soares pregnant	0	167	0.15	1	
uterus NbHPU Homo ...					
gi 955649 dbj D53...Human fetal brain cDNA 5'-end	0	138	0.98	1	
GEN-119A08.					
gi 944552 gb R861...yp88b05.r1 Homo sapiens cDNA	0	136	0.998	1	
clone 194481 5' ...					
gi 1698279 gb AA1...zl02e06.s1 Soares pregnant	0	137	0.9997	1	
uterus NbHPU Homo ...					
gi 1978267 gb AA3...EST29113 Cerebellum II Homo	0	131	0.99991	1	
sapiens cDNA 5' end					

gene

gi 35665 emb X524...	H.sapiens DNA for prointerleukin 1beta, exon 7	0	202	0.0038	1
gi 2169701 dbj E0...	Decombinant DNA encoding hybride poly peptide...	0	206	0.0059	1
gi 1567201 emb A3...	Synthetic human IL-1 beta gene	0	200	0.0073	1
gi 1567203 emb A3...	Synthetic human IL-1 beta gene	0	200	0.0073	1
gi 208634 gb M155...	Synthetic human interleukin 1-beta (IL1B) mRN...	0	206	0.0080	1
gi 2169844 dbj E0...	cDNA encoding human interleukin-1	0	206	0.0095	1
gi 1567287 emb A3...	Synthetic (126Ala,128Ala) IL-1 beta gene	0	197	0.010	1
gi 33789 emb X025...	Human mRNA for interleukin 1 beta. Peripheral...	0	206	0.010	1
gi 2168898 dbj E0...	cDNA encoding human interleukin-1	0	206	0.010	1
gi 208636 gb M350...	Human growth hormone/interleukin 1-beta fusio...	0	200	0.010	1
gi 313969 gb I002...	Sequence 2 from Patent US 4898818	0	206	0.011	1
gi 514106 emb A21...	pGIF- alpha	0	206	0.011	1
gi 2169489 dbj E0...	cDNA encoding a polypeptide,GIF precursor hav...	0	206	0.011	1
gi 313921 gb I011...	Sequence 1 from Patent US 4762914	0	206	0.011	1
gi 35662 emb X560...	Human mRNA for prointerleukin 1 beta.	0	206	0.011	1
gi 186268 gb K027...	Human monocyte interleukin 1 (IL-1) mRNA, com...	0	206	0.011	1
gi 186287 gb M549...	Human monocyte interleukin mRNA, complete cds.	0	206	0.011	1
gi 186283 gb M153...	Human interleukin 1-beta (IL1B) mRNA, complet...	0	206	0.011	1
gi 589345 gb I079...	Sequence 1 from Patent EP 0161901	0	206	0.011	1
gi 2169107 dbj E0...	cDNA sequence for human IL-1	0	206	0.011	1
gi 269368 gb I007...	Sequence 2 from Patent US 4766069	0	206	0.011	1
gi 186281 gb M158...	Human interleukin 1-beta (IL1B) gene, complet...	0	203	0.019	1
gi 33788 emb X045...	Human gene for prointerleukin 1	0	202	0.022	1

 This BLAST Search was run Jun 23 1997 14:05:26

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
 Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
 Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to
 find
 nearly identical sequences rapidly. To identify weak similarities encoded in
 nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= ~~EPIDELTA~~
 (470 letters)

Database: /usr/users/gcgdata/gcgblast/estg
 888,004 sequences; 326,874,798 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

 from this report into SPRI/XREFdb

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
GB_EST7:W08205...W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus ...		0	1410	7.1e-58	1
GB_EST8:W78043...W78043 zd72d01.r1 Soares fetal heart NbHH19W ...		0	439	4.5e-14	1
GB_EST7:W20594...W20594 mc16c06.r1 Soares mouse p3NMF19.5 Mus ...		0	400	3.2e-12	1
GB_EST2:R50241...R50241 yj58a03.r1 Homo sapiens cDNA clone 152...		0	395	6.7e-12	1
GB_EST2:R46871...R46871 yj54f05.r1 Homo sapiens cDNA clone 152...		0	385	2.1e-11	1
GB_EST7:W13935...W13935 mb23a07.r1 Soares mouse p3NMF19.5 Mus ...		0	149	0.96	1

 [Entrez][Return to the top of this page]

>GB_EST7:W08205 W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus musculus cDNA
 clone 332733 5' similar to PIR:A49031 A49031 interleukin 1

receptor

antagonist - mouse ;. 9/96
 Length = 382

gi 198389 gb M631...	M.musculus interleukin 1 receptor antagonist ...	0	442	4.2e-14	1
gi 204928 gb M631...	Rat interleukin 1 receptor antagonist gene, c...	0	433	1.0e-13	1
gi 32578 emb X532...	H.sapiens mRNA for IRAP	0	446	1.2e-13	1
gi 32576 emb X520...	H.sapiens mRNA for interleukin-1 receptor ant...	0	446	1.2e-13	1
gi 198298 gb M575...	Mouse interleukin 1 receptor antagonist (IL1R...	0	442	1.7e-13	1
gi 198387 gb M742...	Mouse IL-1rn antagonist protein mRNA, complet...	0	442	1.9e-13	1
gi 198296 gb M644...	Mus domesticus interleukin 1 receptor antagon...	0	442	2.0e-13	1
gi 1313894 gb L38...	Sus scrofa (clone p0328w) IRAP1 mRNA, complet...	0	397	4.1e-12	1
gi 33798 emb X645...	H.sapiens gene for interleukin-1 receptor ant...	0	392	5.6e-11	1
gi 487864 gb L328...	Mouse germline interleukin 1 receptor antagon...	0	379	2.1e-10	1

[Entrez][Return to the top of this page]

>gi|545740|gb|S68977|S68977 sIL-1ra=interleukin-1 receptor antagonist secreted
form [rabbits, colon tissue, mRNA, 574 nt]
Length = 574

Plus Strand HSPs:

Score = 476 (71.4 bits), Expect = 1.1e-15, P = 1.1e-15

Identities = 196/283 (69%), Positives = 196/283 (69%), Strand = Plus / Plus

Query: 147 GGCACCTGGATGCCAGTCTGTCCCTGTTCATCCTGGGCGTTCA-AGGAGGAAGCCAGTGCC 205
G C CT GA GCC TC G C CCTGT TCCTGGGC T CA AGG GGAAG GTGCC

Sbjct: 255 GCCCCTTGA-GCC--TCAG-CTCCTGT--TCCTGGGCATCCAGAGGGGGAAGTT-GTGCC 307

Query: 206 TATCTTGTGGGA---CAGAGAA-AGGGCCAATTCTGAACTTGAGCCAGTGAACATCATG 261
T TCTTGTG GA C G G A A G AA CT A T GAG C GT AACATCA

Sbjct: 308 TGTCTTGTGTGAAGTCTGGGGATAAGATGAAG-CTCCATTTGGAGGCCGTTAACATCACT 366

Query: 262 GAGCTCTACCTCGGGGCCAAGGA--ATCA-AAGAGCTTCACCTTCTACCGGCGGGATATG 318
GA C CT C G CAAGGA A A AAG GCTTCACCTTC CCG ATA

Sbjct: 367 GA-C-CTGGG-CAAGACAAGGAGCAGGACAAGCGCTTCACCTTCATCCGCTCCAATAGT 423

Query: 319 GGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCTCTGCACCTACCG 378
GG C TACC CCA CTTCGA TC GC CCT CCC GGCTGGTT CTCTGCAC C C G

Sbjct: 424 GGCCCTACCACCACCTTCGAGTCTGCCTCCTGCCCCGGCTGGTTTCTCTGCACGGCCCTG 483

Query: 379 GAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCC-TGG 429
GA GCTGACCAGCC GTCAG CTCAC A A CCC GA GAC CC C TGG

Sbjct: 484 GAGGCTGACCAGCCGGTCAGCCTACCAACACCCCGGACGACTCCATCGTGG 535

SPRI/XREFdb BLAST Report xrBLAST1048889160_0

This BLAST Search was run Sep 9 1997 18:00:45

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find
nearly identical sequences rapidly. To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= (219 letters)

Database: /data/datasets/nt

349,525 sequences; 540,957,745 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
AD gil33798 emb X64532 HSIL1RECA	H.sapiens gene for interleukin-1 receptor ant...	0	259	6.3e-05	1
gil2303331 emb A50276 A50276	Sequence.10 from Patent WO9612022	0	239	7.3e-05	1
gil2303056 emb A49726 A49726	Sequence 1 from Patent WO9609323 >gil2303291 ...	0	239	0.00011	1
gil587699 gb I09591	Sequence 1 from Patent WO 8911540	0	239	0.00012	1
gil587700 gb I09592	Sequence 3 from Patent WO 8911540	0	239	0.00012	1
gil1008970 emb X84348 HSIL1RAI	H.sapiens mRNA for intracellular IL-1 recepto...	0	239	0.00015	1
gil2303333 emb A50279 A50279	Sequence 13 from Patent WO9612022	0	239	0.00015	1
gil587702 gb I09594	Sequence 8 from Patent WO 8911540 >gil589153 ...	0	239	0.00016	1
gil186291 gb M55646 HUMIL1RAA	Human icIL-1ra mRNA, complete cds.	0	239	0.00016	1
gil186385 gb M63099 HUMILRA	Human interleukin 1 receptor antagonist (IL1R...	0	230	0.00034	1
gil32578 emb X53296 HSI1RAP	H.sapiens mRNA for IRAP	0	239	0.00039	1
gil32576 emb X52015 HSI1RA	H.sapiens mRNA for interleukin-1 receptor ant...	0	239	0.00040	1
gil1567289 emb A32118 A32118	Synthetic (50Gly,51Gly) IL-1 beta gene	0	206	0.0036	1
gil1567283 emb A32000 A32000	Synthetic IL-1 beta gene	0	206	0.0037	1

SPRI/XREFdb BLAST Report xrBLAST4724426269_0

This BLAST Search was run Sep 9 1997 17:56:23

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
 Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= (470 letters)

Database: /data/datasets/nt

349,525 sequences; 540,957,745 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gil545740 gb S68977 S68977	sIL-1ra=interleukin-1 receptor antagonist sec...	0	<u>476</u>	1.2e-15	1
gil425787 dbj D21832 RAB11RA1	Rabbit mRNA for interleukin 1 receptor antago...	0	<u>467</u>	1.3e-14	1
gil165436 gb M57526 RAB11RAB	Rabbit interleukin 1 receptor antagonist (IL1...	0	<u>467</u>	1.3e-14	1
gil186291 gb M55646 HUMIL1RAA	Human icIL-1ra mRNA, complete cds.	0	<u>446</u>	2.6e-14	1
gil587702 gb I09594	Sequence 8 from Patent WO 8911540 >gil589153 ...	0	<u>446</u>	2.6e-14	1
gil2303333 emb A50279 A50279	Sequence 13 from Patent WO9612022	0	<u>446</u>	2.7e-14	1
gil1008970 emb X84348 HSIL1RAII	H.sapiens mRNA for intracellular IL-1 recepto...	0	<u>446</u>	2.7e-14	1
gil587699 gb I09591	Sequence 1 from Patent WO 8911540	0	<u>446</u>	2.9e-14	1
gil587700 gb I09592	Sequence 3 from Patent WO 8911540	0	<u>446</u>	2.9e-14	1
gil186385 gb M63099 HUMILRA	Human interleukin 1 receptor antagonist (IL1R...	0	<u>446</u>	2.9e-14	1
gil2303056 emb A49726 A49726	Sequence 1 from Patent WO9609323 >gil2303291 ...	0	<u>446</u>	2.9e-14	1
gil2303331 emb A50276 A50276	Sequence 10 from Patent WO9612022	0	<u>446</u>	3.3e-14	1
gil238584 gb S64082 S64082	interleukin 1 receptor antagonist protein [mi...	0	<u>442</u>	4.3e-14	1

gi 198389 gb M63100 MUSILRA	M.musculus interleukin 1 receptor antagonist ...	0	442	4.5e-14	1
gi 204928 gb M63101 RATILRA	Rat interleukin 1 receptor antagonist gene, c...	0	433	1.1e-13	1
gi 32578 embl X53296 HSIIRAP	H.sapiens mRNA for IRAP	0	446	1.3e-13	1
gi 32576 embl X52015 HSIIRA	H.sapiens mRNA for interleukin-1 receptor ant...	0	446	1.3e-13	1
gi 198298 gb M57525 MUSIL1RAA	Mouse interleukin 1 receptor antagonist (IL1R...	0	442	1.8e-13	1
gi 198387 gb M74294 MUSIL1RN	Mouse IL-1rn antagonist protein mRNA, complet...	0	442	2.1e-13	1
gi 198296 gb M64404 MUSIL1RA	Mus domesticus interleukin 1 receptor antagon...	0	442	2.1e-13	1
gi 1313894 gb L38849 PIGIRAP	Sus scrofa (clone p0328w) IRAP1 mRNA, complet...	0	397	4.5e-12	1
gi 33798 embl X64532 HSIL1RECA	H.sapiens gene for interleukin-1 receptor ant...	0	392	6.1e-11	1
gi 487864 gb L32838 MUSIL1RN	Mouse germline interleukin 1 receptor antagon...	0	379	2.2e-10	1

[Entrez] [Return to the top of this page]

>gi|545740|gb|S68977|S68977 sIL-1ra=interleukin-1 receptor antagonist secreted form [rabbits, colon tissue, mRNA, 574 nt]
Length = 574

Plus Strand HSPs:

Score = 476 (71.4 bits), Expect = 1.2e-15, P = 1.2e-15

Identities = 196/283 (69%), Positives = 196/283 (69%), Strand = Plus / Plus

```

Query:   147 GGCAGTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCA-AGGAGGAAGCCAGTGCC 205
          G C CT GA GCC TC G C CCTGT TCCTGGGC T CA AGG GGAAG GTGCC
Sbjct:   255 GCCCCTTGA-GCC--TCAG-CTCCTGT--TCCTGGGCATCCAGAGGGGGAAGTT-GTGCC 307

Query:   206 TATCTTGTGGGA---CAGAGAA-AGGGCCAATTCTGAAACTTGAGCCAGTGAACATCATG 261
          T TCTTGTG GA C G G A A G AA CT A T GAG C GT AACATCA
Sbjct:   308 TGTCTTGTGTGAAGTCTGGGGATAAGATGAAG-CTCCATTGAGGCGGTTAACATCACT 366

Query:   262 GAGCTCTACCTCGGGGCCAAGGA--ATCA-AAGAGCTTCACCTTCTACCGGCGGGATATG 318
          GA C CT C G CAAGGA A A AAG GCTTCACCTTC CCG ATA
Sbjct:   367 GA-C-CTGGG-CAAGAACAAGGAGCAGGACAAGCGCTTCACCTTCATCCGCTCCAATAGT 423

Query:   319 GGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCTCTGCACCTCACCG 378
          GG C TACC CCA CTTCGA TC GC CCT CCC GGCTGGTT CTCTGCAC C C G
Sbjct:   424 GGCCCTACCACACCTTCGAGTCTGCCTCCTGCCCCGGGCTGGTTTCTCTGCACGGCCCTG 483

Query:   379 GAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCC-TGG 429
          GA GCTGACCAGCC GTCAG CTCAC A A CCC GA GAC CC C TGG
Sbjct:   484 GAGGCTGACCAGCCGGTCAGCCTCACCAACACCCCGGACGACTCCATCGTGG 535

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SPRI/XREFdb BLAST Report xrBLAST3186340332_0

This BLAST Search was run Sep 9 1997 20:09:02

BLASTN 2.0a8MP-WashU [25-Feb-1997] [Build 20:09:57 Feb 25 1997]

Reference: Gish, Warren (1994-1997). unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Notice: this program and its default parameter settings are optimized to find nearly identical sequences rapidly. To identify weak similarities encoded in nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query=  (470 letters)

Database: /data/datasets/est

1,182,287 sequences; 435,520,876 total letters.

Searching....10....20....30....40....50....60....70....80....90....100% done

	Sequences Producing High Segment Pairs	Frame	Score	P(N)	N
gi1282415 gb W08205 W08205	mb49b11.r1 Soares mouse p3NMF19.5 Mus musculu...	0	1410	9.4e-58	1
gi1388557 gb W78043 W78043	zd72d01.r1 Soares fetal heart NbHH19W Homo sa...	0	439	5.9e-14	1
gi1297494 gb W20594 W20594	mc16c06.r1 Soares mouse p3NMF19.5 Mus musculu...	0	400	4.2e-12	1
gi12143 gb R50241 R50241	yj58a03.r1 Homo sapiens cDNA clone 152908 5' ...	0	395	8.9e-12	1
gi1806268 gb R46871 R46871	yj54f05.r1 Homo sapiens cDNA clone 152577 5' ...	0	385	2.7e-11	1
gi1287978 gb W13935 W13935	mb23a07.r1 Soares mouse p3NMF19.5 Mus musculu...	0	149	0.99	1

[Entrez] [Build a Contig] [Return to the top of this page]

>gi1282415|gb|W08205|W08205 mb49b11.r1 Soares mouse p3NMF19.5 Mus musculus
cDNA clone 332733 5' similar to PIR:A49031 A49031 interleukin 1
receptor antagonist - mouse ;
Length = 382

Plus Strand HSPs:

Score = 1410 (211.6 bits), Expect = 9.4e-58, P = 9.4e-58
Identities = 282/282 (100%), Positives = 282/282 (100%), Strand = Plus / Plus